Amendments to the claims:

1. (Previously Presented) A method for identifying multiple different activated transcription factors in a cell sample, the method comprising:

transducing or transfecting a cell sample with a library of constructs, each construct comprising

a cis element sequence comprising at least one copy of a cis element to which a transcription factor is known to bind, the cis element sequence varying within the library of constructs,

a promoter sequence 3' relative to the cis element sequence, and

a reporter sequence 3' relative to the promoter sequence that comprises a variable sequence that varies within the library,

wherein each cis element sequence corresponds to a given reporter sequence within the library of constructs;

expressing the library of constructs in transfected or transduced cell sample to form mRNA transcription products by those of the transduced or transfected cells in which an activated transcription factor is present that binds to the cis element of the construct present in the cell and activates transcription of the reporter sequence of the construct present in the cell;

determining which reporter sequences encode the mRNA transcription products;

identifying the cis elements that correspond to their respective reporter sequences encoding the mRNA transcription products; and

determining which activated transcription factors are present in the cell sample based on the identified cis elements.

2. (Original) A method according to claim 1 wherein the library of cells comprises at least 10 different cis elements.

3. (Original) A method according to claim 1 wherein the library of cells comprises at least 20 different cis elements.

4. (Original) A method according to claim 1 wherein the library of cells comprises at least 50 different cis elements.

5. (Original) A method according to claim 1 wherein the library of cells comprises at least 100 different cis elements.

6. (Original) A method according to claim 1 wherein the cis element sequence comprises at least two copies of the cis element.

7. (Original) A method according to claim 1 wherein the cis element sequence comprises at least three copies of the cis element.

8. (Original) A method according to claim 1 wherein the cis element sequence comprises at least four copies of the cis element.

9. (Original) A method according to claim 1 wherein an individual copy of the cis element has a length between about 5 and 100 base pairs.

10. (Original) A method according to claim 1 wherein an individual copy of the cis element has a length between about 5 and 75 base pairs.

11. (Original) A method according to claim 1 wherein an individual copy of the cis element has a length between about 5 and 50 base pairs.

12. (Original) A method according to claim 1 wherein the variable sequence of the reporter sequence is at least 15 bases in length.

13. (Original) A method according to claim 1 wherein the variable sequence of the reporter sequence is at least 25 bases in length.

14. (Original) A method according to claim 1 wherein the variable sequence of the reporter sequence is at least 50 bases in length.

15. (Original) A method according to claim 1 wherein the variable sequence of the reporter sequence is between 15 and 2000 bases in length.

16. (Original) A method according to claim 1 wherein the variable sequence of the reporter sequence is between 25 and 2000 bases in length.

17. (Original) A method according to claim 1 wherein the variable sequence of the reporter sequence is between 50 and 2000 bases in length.

18. (Original) A method according to claim 1 wherein the cell sample comprises mammalian cells.

19. (Original) A method according to claim 1 wherein the cell sample was obtained from a human.

20. (Canceled without Prejudice)

21. (Original) A method according to claim 20 wherein the library of cells comprises at least 10 different reporter sequences.

22. (Original) A method according to claim 20 wherein the library of cells comprises at least 20 different reporter sequences.

23. (Original) A method according to claim 20 wherein the library of cells comprises at least 50 different reporter sequences.

24. (Previously presented) A method according to claim 1 wherein determining which of the reporter sequences were transcribed comprises reverse transcribing the mRNA transcription products to form cDNA and determining which of the reporter sequences or complements thereof are comprised within the cDNA.

25. (Withdrawn) A method according to claim 24 wherein the reporter sequences comprise priming sequences 5' and 3' relative to the variable sequences, the method further comprising amplifying the cDNA.

26. (Withdrawn) A method according to claim 24 wherein determining which of the reporter sequences or complements thereof are comprised within the cDNA comprises sequencing the cDNA.

27. (Withdrawn) A method according to claim 24 wherein determining which of the reporter sequences or complements thereof are comprised within the cDNA comprises performing a hybridization assay using a library of hybridization probes to detect the reporter sequences and/or or complements thereof.

28. (Withdrawn) A method according to claim 27 wherein the library of hybridization probes are immobilized in an array.

29. (Previously presented) A method according to claim 1, further comprising:

expressing the mRNA transcription products to produce reporter proteins, wherein determining which reporter sequences encode the mRNA transcription products comprising determining which of the reporter proteins were expressed.

30. (Original) A method according to claim 29 wherein determining which of the reporter proteins were expressed comprises employing a library of antibodies capable of binding to the reporter proteins to detect the expressed reporter proteins.

31. (Original) A method according to claim 30 wherein the library of antibodies are immobilized in an array.

32-46. (Canceled without Prejudice)

47. (Withdrawn) A method according to claim 1, further comprising:

using the combination of multiple different activated transcription factors determined as being present in the cell sample to identify the cell type of the cell sample.

48. (Withdrawn) A method according to claim 47, wherein using the identified combination of multiple different activated transcription factors comprises comparing the identified combination of multiple different activated transcription factors to combinations of different activated transcription factors known to be present in known cell types.

49. (Withdrawn) A method according to claim 48, wherein the known cell types comprise diseased and/or healthy cells of a given cell type.

50. (Withdrawn) A method according to claim 1, further comprising:

comparing the combination of multiple different activated transcription factors determined as being present in a cell sample to combinations of multiple different activated transcription factors known to be present in diseased and healthy cell samples.